

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Dalla-Favera, Riccardo

(ii) TITLE OF INVENTION: IDENTIFICATION OF GENES ALTERED IN  
MULTIPLE MYELOMA

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(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

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(A) ADDRESSEE: Cooper & Dunham LLP

(B) STREET: 1185 Avenue of the Americas

(C) CITY: New York

(D) STATE: New York

(E) COUNTRY: U.S.A.

(F) ZIP: 10036

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

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(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 28-MAY-1996

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(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White, John P.

(B) REGISTRATION NUMBER: 28,678

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(C) REFERENCE/DOCKET NUMBER: 50995

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 278-0400

(B) TELEFAX: (212) 391-0525

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Lys Leu Arg Gln Trp Leu Ile Asp Gln Ile Asp Ser Gly Lys Tyr Pro  
1 5 10 15

Gly Leu Val Trp Glu Asn Glu Glu Lys Ser Ile Phe Arg Ile Pro Trp  
20 25 30

Lys His Ala Gly Lys Gln Asp Tyr Asn Arg Glu Glu Asp Ala Ala Leu  
35 40 45

Phe Lys Ala Trp Ala Leu Phe Lys Gly Lys Phe Arg Glu Gly Ile Asp  
50 55 60

Lys Pro Asp Pro Pro Thr Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn  
65 70 75 80

Lys Ser Asn Asp Phe Glu Glu Leu Val Glu Arg Ser Gln Leu Asp Ile  
85 90 95

Ser Asp Pro Tyr Lys Val Tyr Arg Ile Val Pro Glu  
100 105

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

10 Lys Leu Arg Gln Trp Leu Ile Asp Gln Ile Asp Ser Gly Lys Tyr Pro  
1 5 10 15

Gly Leu Val Trp Glu Asn Glu Glu Lys Ser Val Phe Arg Ile Pro Trp  
20 25 30

15 Lys His Ala Gly Lys Gln Asp Tyr Asn Arg Glu Glu Asp Ala Ala Leu  
35 40 45

Phe Lys Ala Trp Ala Leu Phe Lys Gly Lys Phe Arg Glu Gly Ile Asp  
20 50 55 60

Lys Pro Asp Pro Pro Thr Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn  
65 70 75 80

25 Lys Ser Asn Asp Phe Glu Glu Leu Val Glu Arg Ser Gln Leu Asp Ile  
85 90 95

Ser Asp Pro Tyr Lys Val Tyr Arg Ile Val Pro Glu  
100 105

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

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(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5 Arg Met Arg Pro Trp Leu Glu Met Gln Ile Asn Ser Asn Gln Ile Pro  
1 5 10 15

Gly Leu Ile Trp Ile Asn Lys Glu Glu Met Ile Phe Gln Ile Pro Trp  
20 25 30

10 Lys His Ala Ala Lys His Gly Trp Asp Ile Asn Lys Asp Ala Cys Leu  
35 40 45

Phe Arg Ser Trp Ala Ile His Thr Gly Arg Tyr Lys Ala Gly Glu Lys  
50 55 60

15 Glu Pro Asp Pro Lys Thr Trp Lys Ala Asn Phe Arg Cys Ala Met Asn  
65 70 75 80

Ser Leu Pro Asp Ile Glu Glu Val Lys Asp Gln Lys Arg Asn Lys Gly  
85 90 95

20 Ser Ser Ala Val Arg Val Tyr Arg Met Leu Pro Pro  
100 105

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 Arg Met Arg Pro Trp Leu Glu Glu Gln Ile Asn Ser Asn Thr Ile Pro  
1 5 10 15

Gly Leu Lys Trp Leu Asn Lys Glu Lys Lys Ile Phe Gln Ile Pro Trp

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(2) INFORMATION FOR SEQ ID NO:5:

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(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Leu Arg Gln Trp Leu Ile Glu Gln Ile Asp Ser Ser Met Tyr Pro  
1 5 10 15

35

Gly Leu Ile Trp Glu Asn Glu Glu Lys Ser Met Phe Arg Ile Pro Trp  
20 25 30

40

Lys His Ala Gly Lys Gln Asp Tyr Asn Gln Glu Val Asp Ala Ser Ile  
35 40 45

Phe Lys Ala Trp Ala Val Phe Lys Gly Lys Phe Lys Glu Gly Asp Lys

50

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Ala Glu Pro Ala Thr Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn Lys  
65 70 75 80

5

Ser Pro Asp Phe Glu Glu Val Thr Asp Arg Ser Gln Leu Asp Ile Ser  
85 90 95

10

Glu Pro Tyr Lys Val Tyr Arg Ile Val Pro Glu  
100 105

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Leu Arg Asn Trp Val Val Glu Gln Val Glu Ser Gly Gln Phe Pro  
1 5 10 15

30

Gly Val Cys Trp Asp Asp Thr Ala Lys Thr Met Phe Arg Ile Pro Trp  
20 25 30

Lys His Ala Gly Lys Gln Asp Phe Arg Glu Asp Gln Asp Ala Ala Phe  
35 40 45

35

Phe Lys Ala Trp Ala Ile Phe Lys Gly Lys Tyr Lys Glu Gly Asp Thr  
50 55 60

40

Gly Gly Pro Ala Val Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn Lys  
65 70 75 80

Ser Ser Glu Phe Lys Glu Val Pro Glu Arg Gly Arg Met Asp Val Ala

85

90

95

Glu Pro Tyr Lys Val Tyr Gln Leu Leu Pro Pro  
100 105

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

10

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20

Arg Ile Leu Pro Trp Leu Val Ser Gln Leu Asp Leu Gly Gln Leu Glu  
1 5 10 15

25

Gly Val Ala Trp Val Asn Lys Ser Arg Thr Arg Phe Arg Ile Pro Trp  
20 25 30

Lys His Gly Leu Arg Gln Asp Ala Gln Gln Glu Asp Phe Gly Ile Phe  
35 40 45

30

Gln Ala Trp Ala Glu Ala Thr Gly Ala Tyr Val Pro Gly Arg Asp Lys  
50 55 60

Pro Asp Leu Pro Thr Trp Lys Arg Asn Phe Arg Ser Ser Ala Leu Asn  
65 70 75 80

35

Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg Ser Lys Asp Pro His  
85 90 95

40

Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Arg Leu Cys Gln Ser Thr Ile Tyr Trp Asp Gly Pro Leu Ala Leu  
1 5 10 15

Cys Asn Asp Arg Pro Asn Lys Leu Glu Arg Asp Gln Thr Cys Lys Leu  
20 25 30

Phe Asp Thr Gln Gln Phe Leu Ser Glu Leu Gln Ala Phe Ala His His  
35 40 45

Gly Arg Ser Leu Pro Arg Phe Gln Val Thr Leu Cys Phe Gly Glu Glu  
50 55 60

Phe Pro Asp Pro Gln Arg Gln Arg Lys Leu Ile Thr Ala His Val Glu  
65 70 75 80

Pro Leu Leu Ala Arg Gln Leu Tyr Tyr Phe Ala Gln Gln Asn Ser  
85 90 95

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

5           Lys Arg Leu Cys Gln Ser Arg Ile Tyr Trp Asp Gly Pro Leu Ala Leu  
          1                   5                   10                   15

          Cys Ser Asp Arg Pro Asn Lys Leu Glu Arg Asp Gln Thr Cys Lys Leu  
                  20                   25                   30

10          Phe Asp Thr Gln Gln Phe Leu Ser Glu Leu Gln Val Phe Ala His His  
                  35                   40                   45

          Gly Arg Pro Ala Pro Arg Phe Gln Val Thr Leu Cys Phe Gly Glu Glu  
                  50                   55                   60

15          Phe Pro Asp Pro Gln Arg Gln Arg Lys Leu Ile Thr Ala His Val Glu  
                  65                   70                   75                   80

          Pro Leu Leu Ala Arg Gln Leu Tyr Tyr Phe Ala Gln Gln Asn Thr  
20                           85                   90                   95

(2) INFORMATION FOR SEQ ID NO:10:

25          (i) SEQUENCE CHARACTERISTICS:  
            (A) LENGTH: 96 amino acids  
            (B) TYPE: amino acid  
            (C) STRANDEDNESS: single  
            (D) TOPOLOGY: linear

30          (ii) MOLECULE TYPE: peptide

35          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

          Lys Arg Leu Cys Gln Gly Arg Val Phe Cys Ser Gly Asn Ala Val Val  
          1                   5                   10                   15

40          Cys Lys Gly Arg Pro Asn Lys Leu Glu Arg Asp Glu Val Val Gln Val  
                  20                   25                   30

Phe Asp Thr Ser Gln Phe Phe Arg Glu Leu Gln Gln Phe Tyr Asn Ser  
35 40 45

Gln Gly Arg Leu Pro Asp Gly Arg Val Val Leu Cys Phe Gly Glu Glu  
5 50 55 60

Phe Pro Asp Met Ala Pro Leu Arg Ser Lys Leu Ile Leu Val Gln Ile  
65 70 75 80

10 Glu Gln Leu Tyr Val Arg Gln Leu Ala Glu Glu Ala Gly Lys Ser Cys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:11:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

20

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30

Gln Arg Leu Cys Pro Ile Pro Ile Ser Trp Asn Ala Pro Gln Ala Pro  
1 5 10 15

Pro Gly Pro Gly Pro His Leu Leu Pro Ser Asn Glu Cys Val Glu Leu  
20 25 30

35

Phe Arg Thr Ala Tyr Phe Cys Arg Asp Leu Val Arg Tyr Phe Gln Gly  
35 40 45

Leu Gly Pro Pro Pro Lys Phe Gln Val Thr Leu Asn Phe Trp Glu Glu  
50 55 60

40

Ser His Gly Ser Ser His Thr Pro Gln Asn Leu Ile Thr Val Lys Met  
65 70 75 80

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Glu Gln Ala Phe Ala Arg Tyr Leu Leu Glu Gln Thr Pro Glu Gln Gln  
85 90 95

5 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

20 Gln Arg Leu Gly His Cys His Thr Tyr Trp Ala Val Ser Glu Glu Leu  
1 5 10 15

Leu Pro Asn Ser Gly His Gly Pro Asp Gly Glu Val Pro Lys Asp Lys  
20 25 30

25

Glu Gly Gly Val Phe Asp Leu Gly Pro Phe Ile Val Asp Leu Ile Thr  
35 40 45

30

Phe Thr Glu Gly Ser Gly Arg Ser Pro Arg Tyr Ala Trp Leu Phe Cys  
50 55 60

Val Gly Glu Ser Trp Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val  
65 70 75 80

35

Met Val Lys Val Val Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala  
85 90 95

Arg Val Gly Gly  
100

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 217..1569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCTGACCAA CATGGTAAAA CCCCATCTCT GCTAAACTA CAAAAAATTA GCTGGATGTG  
60

GTGGCAGGGA ACCTGTCATC CCAGCTAGTT GGGAGACTGA GGCAGGAGAA TCGCTCGATC  
120

TTGGGACCCA CCGCTGCCCT CAGCTCCGAG TCCAGGGCGA GTGCAGAGCA CAGCGGGCGG  
180

AGGACCCCGG GCGCGGGCGC GGACGGCACG CGGGGC ATG AAC CTG GAG GGC GGC  
234

Met Asn Leu Glu Gly Gly  
1 5

GGC CGA GGC GGA GAG TTC GGC ATG AGC GCG GTG AGC TGC GGC AAC GGC  
282

Gly Arg Gly Gly Glu Phe Gly Met Ser Ala Val Ser Cys Gly Asn Gly  
10 15 20

AAG CTC CGC CAG TGG CTG ATC GAC CAG ATC GAC AGC GGC AAG TAC CCC  
330

Lys Leu Arg Gln Trp Leu Ile Asp Gln Ile Asp Ser Gly Lys Tyr Pro  
25 30 35

GGG CTG GTG TGG GAG AAC GAG GAG AAG AGC ATC TTC CGC ATC CCC TGG  
378

CAC AAC TAC ATG ATG CCA CCC CTC GAC CGA AGC TGG AGG GAC TAC GTC  
762  
His Asn Tyr Met Met Pro Pro Leu Asp Arg Ser Trp Arg Asp Tyr Val  
170 175 180

CCG GAT CAG CCA CAC CCG GAA ATC CCG TAC CAA TGT CCC ATG ACG TTT  
810

Pro Asp Gln Pro His Pro Glu Ile Pro Tyr Gln Cys Pro Met Thr Phe  
185 190 195

5

GGA CCC CGC GGC CAC CAC TGG CAA GGC CCA GCT TGT GAA AAT GGT TGC  
858

Gly Pro Arg Gly His His Trp Gln Gly Pro Ala Cys Glu Asn Gly Cys  
200 205 210

10

CAG GTG ACA GGA ACC TTT TAT GCT TGT GCC CCA CCT GAG TCC CAG GCT  
906

Gln Val Thr Gly Thr Phe Tyr Ala Cys Ala Pro Pro Glu Ser Gln Ala  
215 220 225 230

15

CCC GGA GTC CCC ACA GAG CCA AGC ATA AGG TCT GCC GAA GCC TTG GCG  
954

Pro Gly Val Pro Thr Glu Pro Ser Ile Arg Ser Ala Glu Ala Leu Ala  
235 240 245

20

TTC TCA GAC TGC CGG CTG CAC ATC TGC CTG TAC TAC CGG GAA ATC CTC  
1002

Phe Ser Asp Cys Arg Leu His Ile Cys Leu Tyr Tyr Arg Glu Ile Leu  
250 255 260

25

GTG AAG GAG CTG ACC ACG TCC AGC CCC GAG GGC TGC CGG ATC TCC CAT  
1050

Val Lys Glu Leu Thr Thr Ser Ser Pro Glu Gly Cys Arg Ile Ser His  
265 270 275

30

GGA CAT ACG TAT GAC GCC AGC AAC CTG GAC CAG GTC CTG TTC CCC TAC  
1098

Gly His Thr Tyr Asp Ala Ser Asn Leu Asp Gln Val Leu Phe Pro Tyr  
280 285 290

35

CCA GAG GAC AAT GGC CAC AGG AAA AAC ATT GAG AAC CTG CTG AGC CAC  
1146

Pro Glu Asp Asn Gly His Arg Lys Asn Ile Glu Asn Leu Leu Ser His  
295 300 305 310

40

CTG GAG AGG GGC GTG GTC CTC TGG ATG GCC CCC GAC GGG CTC TAT GCG  
1194

Leu Glu Arg Gly Val Val Leu Trp Met Ala Pro Asp Gly Leu Tyr Ala  
315 320 325

5 AAA AGA CTG TGC CAG AGC ACG ATC TAC TGG GAC GGG CCC CTG GCG CTG  
1242

Lys Arg Leu Cys Gln Ser Thr Ile Tyr Trp Asp Gly Pro Leu Ala Leu  
330 335 340

10 TGC AAC GAC CGG CCC AAC AAA CTG GAG AGA GAC CAG ACC TGC AAG CTC  
1290

Cys Asn Asp Arg Pro Asn Lys Leu Glu Arg Asp Gln Thr Cys Lys Leu  
345 350 355

15 TTT GAC ACA CAG CAG TTC TTG TCA GAG CTG CAA GCG TTT GCT CAC CAC  
1338

Phe Asp Thr Gln Gln Phe Leu Ser Glu Leu Gln Ala Phe Ala His His  
360 365 370

20 GGC CGC TCC CTG CCA AGA TTC CAG GTG ACT CTA TGC TTT GGA GAG GAG  
1386

Gly Arg Ser Leu Pro Arg Phe Gln Val Thr Leu Cys Phe Gly Glu Glu  
375 380 385 390

25 TTT CCA GAC CCT CAG AGG CAA AGA AAG CTC ATC ACA GCT CAC GTA GAA  
1434

Phe Pro Asp Pro Gln Arg Gln Arg Lys Leu Ile Thr Ala His Val Glu  
395 400 405

30 CCT CTG CTA GCC AGA CAA CTA TAT TAT TTT GCT CAA CAA AAC AGT GGA  
1482

Pro Leu Leu Ala Arg Gln Leu Tyr Tyr Phe Ala Gln Gln Asn Ser Gly  
410 415 420

35 CAT TTC CTG AGG GGC TAC GAT TTA CCA GAA CAC ATC AGC AAT CCA GAA  
1530

His Phe Leu Arg Gly Tyr Asp Leu Pro Glu His Ile Ser Asn Pro Glu  
425 430 435

40 GAT TAC CAC AGA TCT ATC CGC CAT TCC TCT ATT CAA GAA TGAAAAATGT  
1579

Asp Tyr His Arg Ser Ile Arg His Ser Ser Ile Gln Glu  
440 445 450

GTCTTGCTCT GTCTCCCAGG CTGGAGTGCA GTGACACAAT CTCAGCTCAC TGTGACCTCC  
1699

10 TGAGCCACTG CACCCACCCA AGACAAGTGA TTTTCATTGT AAATATTTGA CTTTAGTGAA  
1819

15  
AGCGGTTGAG GAGAATTGCG GCGAGACAAG CATGGAAAAT CAGTGACATC TGATTGGCAG  
1939

CATTGATGAT CACTGTGAAA ATTGACCAAG TGATGTGTTT ACATTTACTG AAATGCGCTC  
2059

ACACTGACTA GAGTGATGAC TGCTTGTAGG TATGTCTGTG CCATTTCTCA GGGAAGTAAG  
2179

35 TTCTTTGTGGA AGACACTTGC TGAGTGAAGG AAATGAATCT TTGACTGAAG CCGTGCCTGT  
2299

40 CACCCTCCTT CCCATTGGCT TTCTCTCCTT GGCCTTTCCT GGAAGCCAGT TAGTAAACTT  
2419



CTACAATCTA GTAATGTCTA AGTAATGGTT AAGTTTTCTT GTTCTGTCAT CTTTTTGACC  
2539

10 TCTTAATACT TGAAGTGTG CCCTTCTGTC CAAGTACTTA ACTATCTGTT CCCTTCCTCT  
2659

15  
GAGGAGCCGG GGACTCCCAG GCTGGAGAGC ACTGCCAGGA CCCACCACTG GAAGCAGGAT  
2779

GCTTCCTCGT GCCAATTATA GTTGACAGG GCCTTAAAT TACTTGGCTT TTTCCAAATG  
2899

TTTGTGGTTT TGAGAAAGTA CAGCAGTAGA CTGGGGCGTC ACCTCCAGGC CGTTTCTCAT  
3019

GTGTGTTTCCT GCTTTTCTAA TGGATATTTT AAATTCATTC AACAAGCACC TAGTAAGTGC  
35 3139

40 GAAACATTAT TTTTAAATGT TTAAAAAGTT TCTAATATTA AAGTCAGAAT ATTAATACAA  
3259

TTAATATTAA TATTAAC TAC AGAAAAGACA AACAGTAGAG AACAGCAAAA AAATAAAAAG  
3319

5 GATCTCCTTT TTTCCCAGCC CAAATTCTCC TCTCTAAAAG TGTCCACAAG AAGGGGTGTT  
3379

TATTCTTCCA ACACATTTCA CTTTTCTGTA AATATACATA AACTTAAAAA GAAAACCTCA  
3439

10 TGGAGTCATC TTGCACACAC TTTTCATGCA GTGCTCTTTG TAGCTAAACA GTGAAGATTT  
3499

15 ACCTCGTTCT GCTCAGAGGC CTTGCTGTGG AGCTCCACTG CCATGTACCC AGTAGGGTTT  
3559

GACATTTTCAT TAGCCATGCA ACATGGATAT GTATTGGGCA GCAGACTGTG TTTCGTGAAC  
3619

20 TGCAGTGATG TATACATCTT ATAGATGCAA AGTATTTTGG GGTATATTAT CCTAAGGGAA  
3679

GATAAAGATG ATATTAAGAA CTGCTGTTTC ACGGGGCCCT TACCTGTGAC CCTCTTTGCT  
3739

25 GAAGAATATT TAACCCACACA CAGCACTTCA AAGAAGCTGT CTTGGAAGTC TGTCTCAGGA  
3799

30 GCACCCTGTC TTCTTAATTC TCCAAGCGGA TGCTCCATTT CAATTGCTTT GTGACTTCTT  
3859

CTTCTTTGTT TTTTAAATA TTATGCTGCT TTAACAGTGG AGCTGAATTT TCTGGAAAAT  
3919

35 GCTTCTTGGC TGGGGCCACT ACCTCCTTTC CTATCTTTAC ATCTATGTGT ATGTTGACTT  
3979

TTTAAAATTC TGAGTGATCC AGGGTATGAC CTAGGGAATG AACTAGCTAT GGAAATAACT  
4039

40 CAGGGTTAGG AATCCTAGCA CTTGTCTCAG GACTCTGAAA AGGAACGGCT TCCTCATTC  
4099

TTGTCTTGAT AAAGTGGAAT TGGCAAAC TA GAATTTAGTT TGTACTCAGT GGACAGTGCT  
4159

5 GTTGAAGATT TGAGGACTTG TTAAAGAGCA CTGGGTCATA TGGAAAAAAT GTATGTGTCT  
4219

CCCCAGGTGC ATTTTCTTGG TTTATGTCTT GTTCTTGAGA TTTTGTATAT TTAGGAAAAC  
4279

10 CTCAAGCAGT AATTAATATC TCCTGGAACA CTATAGAGAA CCAAGTGACC GACTCATTTA  
4339

CAACTGAAAC CTAGGAAGCC CCTGAGTCCT GAGCGAAAAC AGGAGAGTTA GTCGCCCTAC  
4399

15 AGAAAACCCA GCTAGACTAT TGGGTATGAA CTAAAAAGAG ACTGTGCCAT GGTGAGAAAA  
4459

20 ATGTAAAATC CTACAGTGGA ATGAGCAGCC CTTACAGTGT TGTTACCACC AAGGGCAGGT  
4519

AGGTATTAGT GTTTGAAAAA GCTGGTCTTT GAGCGAGGGC ATAAATACAG CTAGCCCCAG  
4579

25 GGGTGGAACA ACTGTGGGAG TCTTGGGTAC TCGCACCTCT TGGCTTTGTT GATGCTCCGC  
4639

CAGGAAGGCC ACTTGTGTGT GCGTGTCACT TACTTTTTTA GTAACAATTC AGATCCAGTG  
4699

30 TAAACTTCCG TTCATTGCTC TCCAGTCACA TGCCCCACT TCCCCACAGG TGAAAGTTTT  
4759

35 TCTGAAGTGT TGGGATTGGT TAAGGTCTTT ATTTGTATTA CGTATCTCCC CAAGTCCTCT  
4819

GTGGCCAGCT GCATCTGTCT GAATGGTGCG TGAAGGCTCT CAGACCTTAC ACACCATTTT  
4879

40 GTAAGTTATG TTTTACATGC CCCGTTTTTG AGACTGATCT CGATGCAGGT GGATCTCCTT  
4939

GAGATCCTGA TAGCCTGTGA CAGGAATGAA GTAAAGGTCA GTTTTTTTTGG TATTGATTTT  
4999

5 CACAGCTTTG AGGAACATGC ATAAGAAATG TAGCTGAAGT AGAGGGGACG TGAGAGAAGG  
5059

GCCAGGCCGG CAGGCCAACC CTCCTCCAAT GGAAATTCCC GTGTTGCTTC AAACTGAGAC  
5119

10 AGATGGGACT TAACAGGCAA TGGGGTCCAC TTCCCCCTCT TCAGCATCCC CCGTACC  
5176

(2) INFORMATION FOR SEQ ID NO:14:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 451 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

25 Met Asn Leu Glu Gly Gly Gly Arg Gly Gly Glu Phe Gly Met Ser Ala  
1 5 10 15

Val Ser Cys Gly Asn Gly Lys Leu Arg Gln Trp Leu Ile Asp Gln Ile  
20 25 30

30

Asp Ser Gly Lys Tyr Pro Gly Leu Val Trp Glu Asn Glu Glu Lys Ser  
35 40 45

35

Ile Phe Arg Ile Pro Trp Lys His Ala Gly Lys Gln Asp Tyr Asn Arg  
50 55 60

Glu Glu Asp Ala Ala Leu Phe Lys Ala Trp Ala Leu Phe Lys Gly Lys  
65 70 75 80

40

Phe Arg Glu Gly Ile Asp Lys Pro Asp Pro Pro Thr Trp Lys Thr Arg  
85 90 95

Arg Ser Gln Leu Asp Ile Ser Asp Pro Tyr Lys Val Tyr Arg Ile Val  
115 120 125

Gln Met Ser Met Ser His Pro Tyr Thr Met Thr Thr Pro Tyr Pro Ser  
145 150 155 160

Leu Pro Ala Gln Gln Val His Asn Tyr Met Met Pro Pro Leu Asp Arg  
165 170 175

Ser Trp Arg Asp Tyr Val Pro Asp Gln Pro His Pro Glu Ile Pro Tyr  
180 185 190

Gln Cys Pro Met Thr Phe Gly Pro Arg Gly His His Trp Gln Gly Pro  
195 200 205

Ala Cys Glu Asn Gly Cys Gln Val Thr Gly Thr Phe Tyr Ala Cys Ala  
210 215 220

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Glu | Ser | Gln | Ala | Pro | Gly | Val | Pro | Thr | Glu | Pro | Ser | Ile | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

Ser Ala Glu Ala Leu Ala Phe Ser Asp Cys Arg Leu His Ile Cys Leu  
245 250 255

Tyr Tyr Arg Glu Ile Leu Val Lys Glu Leu Thr Thr Ser Ser Pro Glu  
260 265 270

Gly Cys Arg Ile Ser His Gly His Thr Tyr Asp Ala Ser Asn Leu Asp  
275 280 285

Gln Val Leu Phe Pro Tyr Pro Glu Asp Asn Gly His Arg Lys Asn Ile  
290 295 300

Glu Asn Leu Leu Ser His Leu Glu Arg Gly Val Val Leu Trp Met Ala  
305 310 315 320

Pro Asp Gly Leu Tyr Ala Lys Arg Leu Cys Gln Ser Thr Ile Tyr Trp  
325 330 335

5 Asp Gly Pro Leu Ala Leu Cys Asn Asp Arg Pro Asn Lys Leu Glu Arg  
340 345 350

Asp Gln Thr Cys Lys Leu Phe Asp Thr Gln Gln Phe Leu Ser Glu Leu  
355 360 365

10 Gln Ala Phe Ala His His Gly Arg Ser Leu Pro Arg Phe Gln Val Thr  
370 375 380

Leu Cys Phe Gly Glu Glu Phe Pro Asp Pro Gln Arg Gln Arg Lys Leu  
385 390 395 400

15 Ile Thr Ala His Val Glu Pro Leu Leu Ala Arg Gln Leu Tyr Tyr Phe  
405 410 415

20 Ala Gln Gln Asn Ser Gly His Phe Leu Arg Gly Tyr Asp Leu Pro Glu  
420 425 430

His Ile Ser Asn Pro Glu Asp Tyr His Arg Ser Ile Arg His Ser Ser  
435 440 445

25 Ile Gln Glu  
450

(2) INFORMATION FOR SEQ ID NO:15:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTTTCTCTAC AGTCACCTCC CTGTTTACCA AAGATAATCA CAATAAGTCC AGTTTACTTA  
60

CAAAACAAGT TTAGTTATTA GAGGAACTA AACTTCAGG ATTCAGTCCA GATAATTTT  
5 120

AAAACTCTA AAACAATGGA CAGGGCTAGA AT  
152

10 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGGGCTCGGC CTGGTGGGGC AGCCACAGCG GGACGCAGTA GTGAAAGTCC AGTTTACTTA  
25 60

CAAAACAAGT TTAGTTATTA GAGGAACTA AACTTCAGG ATTCAGCAGG GCATGAGGAG  
120

GCAGCTCCTC ACCCTCCCTT TCTCTTTTGT AC  
152

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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TGGGCTCGGC CTTGGTGGGG CAGCCACAGC GGGACGCAAG TAGTGAGGGC ACTCAGAACG  
60

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CCACTCAGCC CCGACAGGGC ACTCAGAACG CCACTCAGCC CCGACAGGCA GGGCACGAGG  
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AGGCAGCTCC TCACCCTCCC TTTCTCTTTT GT  
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